

WHAT IS CLAIMED IS:

1. An isolated bacterial strain that oxidizes nitrite to nitrate, comprising a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.
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2. The bacterial strain of claim 1, wherein the nucleotide sequence is identical to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.
3. A biologically pure culture of a bacterial strain that oxidizes nitrite to nitrate, wherein the
10 16S rDNA of the bacterial strain has a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.
4. The biologically pure culture of claim 3, wherein the nucleotide sequence is identical to
15 SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.
5. A composition, comprising an isolated bacterial strain that oxidizes nitrite to nitrate, wherein said bacterial strain comprises a nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.
- 20 6. The composition of claim 5, wherein the composition is in a form selected from the group consisting of liquid, frozen, freeze-dried and powdered.
7. The composition of claim 5, wherein the composition is included in a polymer.
8. The composition of claim 7, wherein the polymer is selected from the group consisting of acrylamide, alginate, carrageenan and combinations thereof.

9. The composition of claim 5, further comprising a microorganism selected from the group consisting of ammonia-oxidizing organisms, nitrite-oxidizing microorganisms, nitrate-reducing microorganisms, heterotrophic microorganisms and combinations thereof.

10. A composition, comprising a concentrated bacterial strain that oxidizes nitrite to nitrate wherein the 16S rDNA of the bacterial strain has a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

11. The composition of claim 10, wherein said bacterial strain has a 16S rDNA sequence which is identical to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

12. The composition of claim 10, further comprising a microorganism selected from the group consisting of ammonia-oxidizing organisms, nitrite-oxidizing microorganisms, nitrate-reducing microorganisms, heterotrophic microorganisms and combinations thereof.

13. A composition, comprising at least two isolated bacterial strains that oxidize nitrite to nitrate, wherein each of the at least two bacterial strains have 16S rDNA including a nucleotide sequence independently selected from the group consisting of nucleotide sequences that have at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

14. The composition of claim 13, further comprising a microorganism selected from the group consisting of ammonia-oxidizing organisms, nitrite-oxidizing microorganisms, nitrate-reducing microorganisms, heterotrophic microorganisms and combinations thereof.

15. The composition of claim 13, wherein said at least two bacterial strains include a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:1, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:2, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:3, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:4, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:5, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:6, a

bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:7 and a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:8.

16. The composition of claim 13 created by the process of freeze-drying, wherein the freeze-drying process comprises:

treating the at least two isolated bacterial strains with a cryoprotectant;

placing the treated bacterial strains in a freezer;

removing the treated bacterial strains from the freezer; and

drying the bacterial strains under vacuum pressure.

17. An isolated nucleic acid, comprising a sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

18. The isolated nucleic acid of claim 17, wherein the sequence is identical to a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8.

19. An oligonucleotide probe, comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:18.

20. An oligonucleotide probe that has at least 96% identity over the full length thereof to a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:18, wherein the oligonucleotide probe hybridizes to the nucleic acid of bacteria having 16S rDNA that has a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

21. A polymerase chain reaction (PCR) primer, comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22.

22. A polymerase chain reaction (PCR) primer that has at least 96% identity over the full length thereof to a nucleotide sequence selected from the group consisting of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22, wherein the PCR primer hybridizes to the nucleic acid of bacteria having 16S rDNA that has a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8.

23. A method of alleviating or preventing the accumulation of nitrite in a medium comprising:

providing a bacterial strain that oxidizes nitrite to nitrate, wherein said bacterial strain comprises a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8; and

introducing into the medium an amount of the bacterial strain sufficient to alleviate or prevent the accumulation of nitrite in the medium.

24. The method of claim 23, wherein the medium is selected from the group consisting of a saltwater aquarium, a freshwater aquarium, wastewater and liquid in an aquaculture facility.

25. The method of claim 23, wherein introducing into the medium further comprises placing the bacterial strain into the medium on a vector selected from the group consisting of a rotating biological contactor, a biofilter and a polymer.

26. A method of alleviating or preventing the accumulation of nitrite in a medium, comprising:

providing a bacterial strain that oxidizes nitrite to nitrate, wherein said bacterial strain comprises a nucleotide sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8; and

introducing into the medium an amount of the bacterial strain sufficient to alleviate or prevent the accumulation of nitrite in the medium.

27. A bioremediation process that alleviates or prevents the accumulation of nitrite in a medium, comprising:

5 providing a bacterial strain that oxidizes nitrite to nitrate, wherein said bacterial strain comprises a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8; and

10 introducing into the medium an amount of the bacterial strain sufficient to remediate the medium.

28. A method of alleviating or preventing the accumulation of nitrite in a medium, comprising:

15 providing a composition comprising at least two isolated bacterial strains that oxidize nitrite to nitrate, wherein each of the at least two bacterial strains have 16S rDNA including a nucleotide sequence independently selected from the group consisting of nucleotide sequences that have at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8; and

introducing into the medium an amount of the composition sufficient to alleviate or prevent the accumulation of nitrite in the medium.

20 29. The method of claim 28, wherein the at least two isolated bacterial strains include a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:1, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:2, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:3, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:4, a
25 bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:5, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:6, a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:7

and a bacterial strain with a 16S rDNA including a nucleotide sequence as set forth in SEQ ID NO:8.

30. The method of claim 28, wherein the composition further comprises a microorganism selected from the group consisting of ammonia-oxidizing organisms, nitrite-oxidizing
5 microorganisms, nitrate-reducing microorganisms, heterotrophic microorganisms and combinations thereof.

31. A method for detecting and determining the quantity of bacteria that oxidize nitrite to nitrate in a medium, wherein the 16S rDNA of the bacteria includes a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID
10 NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 and SEQ ID NO:8, comprising:

providing a detectably labeled probe including a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:18;

isolating total DNA from the medium;

15 exposing the isolated total DNA to the detectably labeled probe under conditions under which the probe hybridizes to only the nucleic acid of bacteria having 16S rDNA including the nucleotide sequence; and

detecting and measuring the amount of hybridized probe.

32. The method of claim 31, wherein the medium is selected from the group consisting of a
20 saltwater aquarium, a freshwater aquarium, wastewater and liquid in an aquaculture facility.

33. The method of claim 31, wherein the medium includes therein a material selected from the group consisting of aquarium gravel, filter sponges, filter floss and plastic filter media.

34. The method of claim 33, wherein isolating total DNA from the medium comprises isolating the total DNA from the material.

25 35. The method of claim 31, wherein providing a detectably labeled probe further comprises including the detectably labeled probe on a DNA chip.

36. The method of claim 31, wherein the method incorporates an automated process.

37. The method of claim 36, wherein the automated process is selected from the group consisting of DNA microarray, protein microarray, biosensor, bioprobe, capillary electrophoresis and real time polymerase chain reaction.

38. The method of claim 31, wherein the presence of hybridized probe is indicative of the presence of bacteria that oxidize nitrite to nitrate and the amount of hybridized probe is indicative of the quantity of said bacteria that oxidize nitrite to nitrate in said medium.

39. A method for detecting and determining the quantity of bacteria that oxidize nitrite to nitrate in a medium, wherein the 16S rDNA of the bacteria includes a nucleotide sequence that has at least 96% identity over the full length thereof to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7 or SEQ ID NO:8., comprising:

providing a detectably labeled probe that has at least 96% identity over the full length thereof to a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:18;

isolating total DNA from the medium;

exposing the isolated total DNA to the detectably labeled probe under conditions under which the probe hybridizes to only the nucleic acid of bacteria having 16S rDNA including the nucleotide sequence; and

detecting and measuring the amount of hybridized probe.

40. The method of claim 39 wherein the medium is selected from the group consisting of a saltwater aquarium, a freshwater aquarium, wastewater and liquid in an aquaculture facility.

41. The method of claim 39, wherein the medium includes therein a material selected from the group consisting of aquarium gravel, filter sponges, filter floss and plastic filter media.

42. The method of claim 41 wherein isolating total DNA from the medium comprises isolating the total DNA from the material.

43. The method of claim 39, wherein providing a detectably labeled probe further comprises including the detectably labeled probe on a DNA chip.

44. The method of claim 39, wherein the method incorporates an automated process.

45. The method of claim 44, wherein the automated process is selected from the group consisting of DNA microarray, protein microarray, biosensor, bioprobe, capillary electrophoresis and real time polymerase chain reaction.

5 46. The method of claim 39, wherein the presence of hybridized probe is indicative of the presence of bacteria that oxidize nitrite to nitrate and the amount of hybridized probe is indicative of the quantity of said bacteria that oxidize nitrite to nitrate in said medium.

47. A DNA chip, comprising:

a solid substrate; and

10 an oligonucleotide probe including a nucleotide sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16 and SEQ ID NO:18 configured upon the solid substrate.

48. The DNA chip of claim 47, wherein the probe is attached to the solid substrate by covalent bonding.

15 49. A composition comprising nitrite-oxidizing bacteria and ammonia-oxidizing bacteria, present in an approximately 1:3 ratio, wherein the nitrite-oxidizing bacteria comprises a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:1, a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:2, a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:3, a bacterial
20 strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:4, a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:5, a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:6, a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:7 and a bacterial strain having 16S rDNA including a nucleotide sequence identical to SEQ ID NO:8.

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